

```

> O <
O | 10 IntelliGenetics
> O <

PastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq2-Peptides.res made by tport on Thu 10 Jul 103 11:28:49 - PDT

Query sequence being compared: US-09-508-832-2 (1-110)
Number of sequences searched: 21
Number of scores above cutoff: 21

Results of the initial comparison of US-09-508-832-2 (1-110) with:

```

Results of the initial comparison of US-09-508-832-2 (1-110) with:
E102-10005000022 200

N_pep	Score
0	50
10	12
20	24
30	37
40	49
50	61
60	73
70	76
80	86
90	98
100	100
110	110

STDEV	0	1	2	3
Similarity matrix	PAM-150	K-tuple	1	
Mismatch level of sim.	168			
Mismatch penalty	1	Joining penalty	20	
PARAMETERS				

Gap penalty	5.00	Window size	110
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		
SEARCH STATISTICS			
Scores :	Mean 25	Median 11	Standard Deviation 29.71
Times :	00:00:00.00	00:00:00.00	Total Elapsed 00:00:00.00

Number of residues: 1041
 Number of sequences searched: 21
 Number of scores above cutoff: 21

The scores below are sorted by initial score.
 Significance is calculated based on initial score.
 A 100% identical sequence to the query sequence was found:

60	70	80	90	100	110
RRAQELRRIGDEFNENYTRVYANDYREADHPOMVILQLRFLFLRFLVWRRH					
RRAQELRRIGDEFNENYTRVYANDYREADHPOMVILQLRFLFLRFLVWRRH	150	160	170	180	190
					X

US-09-508-832-2 (1-110)
US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score	=	63	Optimized Score	=	94	S
residue Identity	=	63%	Matches	=	87	M
maps	=	28	Conservative Substitutions			

Initial Identity	=	61	Optimized Score	=	69	Significance	=	1.21
Residue Identity	=	35%	Matches	=	48	Mismatches	=	58
Gaps	=	26	Conservative Substitutions	=	4			

EIWIQAELRRIGDEFNAYARRYARRVFLNNYQAAEDHPRMVILRL
150 160 170 180

60	70	80	90	100	110
RRAQELRRIGDEFNENYTRVYANDYREADHPOMVILQLRFLFRFLVWRRH					
RRAQELRRIGDEFNENYTRVYANDYREADHPOMVILQLRFLFRFLVWRRH	150	160	170	180	190
					X

US-09-508-832-2 (1-110)
US-09-508-832-8 Sequence 8, Application US/09508832

	Optimized	Score	=	94	S
Initial Score =	63				
Residue Identity =	63.8	Matches	=	87	M
Substitutions =	28	Conservative	Substitutions		

Initial Score	=	61	Optimized Score	=	69	Significance	=	1.21
Biodegradable Identity	=	35%	Matches	=	48	Mismatches	=	58
Substitutions	=	26	Conservative Substitutions	=	4		=	4

```

-----RIGIDDEFNETYTRRVFANDYREAEIDHQMQVILQLLFIFRLVWRRH
-----|-----|-----|-----|-----|-----|-----|-----|-----|
-----FATRSPLFIFMRSSLLSRSSGGFSEFDTRSPAPMSCDKSTQPSPPSQAFNHYLSAMASMQAEADMRP
-----80      90      100      110      120      130      140

```

EIWIQAELRRIGDEFNAYARRYFLNNYQAAEDHPRMVLRL
150 160 170 180

PARAMETERS		SEARCH STATISTICS		SEQUENCE ALIGNMENT		SEQUENCE ALIGNMENT	
Similarity matrix	PAM-150	K-tuple	1	Initial Score	112	Optimized Score	177
Threshold level of sim.	168	Joining penalty	1	Residue Identity	86%	Matches	173
Mismatch penalty	1	Window size	20	Gaps	6	conservative substitutions	17
Gap penalty	5.00		110				4
Gap size penalty	0.05						
Cutoff score	3						
Randomization group	0						
Scores :		Mean	Median	Standard Deviation			
		33	11	49.41			
Times :		CPU		Total Elapsed			
		00:00:00.00		00:00:00.00			
Number of residues :		1041			1041		
Number of sequences searched :		21			21		
Number of scores above cutoff :		21					
The scores below are sorted by initial score.							
Significance is calculated based on initial score.							
A 100% identical sequence to the query sequence was found:							
SEQUENCE ALIGNMENT		SEQUENCE ALIGNMENT		SEQUENCE ALIGNMENT		SEQUENCE ALIGNMENT	
Sequence Name	Description	Init. Score	Opt. Score	Length	Score	Sig.	Frame
US-09-508-832-6 (1-196)	Application US/09508832	98	Optimized Score	98	Optimized Score	98	Optimized Score
US-09-508-832-10 Sequence 10, Application US/09508832		73%	Residue Identity	73%	Residue Identity	73%	Residue Identity
		Matches		Matches		Matches	
		Mismatches		Mismatches		Mismatches	
		Significance		Significance		Significance	

> 0 <
> 01 10 IntelliGenetics
> 0 <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file seq1-Nucs.res made by tport on Thu 10 Jul 103 11:15:13 -PDT.
Query sequence being compared: US-09-508-832-1 (1-332)
Number of sequences searched: 18
Number of scores above cutoff: 18
Results of the initial comparison of US-09-508-832-1 (1-332) with:
File : US0950832.seq

Results of the initial comparison of US-09-508-832-1 (1-332) with
File : US09508832.seq

SCCSCORE	STDEV	Solid Line (Asterisks)	Dashed Line (Double Asterisks)
0	0	100-	100-
37	37	50-	50-
74	74	100-	100-
111	111	100-	100-
148	148	100-	100-
184	184	100-	100-
221	221	100-	100-
258	258	100-	100-
295	295	100-	100-
332	332	100-	100-

PARAMETERS		SEARCH STATISTICS			SIGNIFICANCE	
Similarity matrix	Unitary	K-tuple			Init. Score	Opt. Score
Mismatch penalty	1	Joining	penalty		Length	Significance
Gap penalty	5.00	Window	size			
Gap size penalty	0.33					
Cutoff score	1					
Randomization group	0					
Scores:		Mean	Median	Standard Deviation	P-value	
Times:	00:00:00.00	CPU	67	15	98.37	
Number of residues:					2713	
Number of sequences searched:					18	
Number of scores above cutoff:					18	

Sequence Name	Description	Length	Init.	Opt.	Score	Sig.	Frame
1. US-09-508-832-1	Sequence 1, Application US	332	332	332	2.69	0	
2. US-09-508-832-3	Sequence 3, Application US	422	209	298	1.44	0	
3. US-09-508-832-5	Sequence 5, Application US	590	209	245	1.44	0	
4. US-09-508-832-7	Sequence 7, Application US	416	151	240	0.85	0	
5. US-09-508-832-9	Sequence 9, Application US	596	151	193	0.85	0	

500 TATTCTGAAATAATACCAAGCAGCGAAGAACCCACGAATGGTTACCTTACGACTGTACGTACATG
510 520 530 540 550 560 570
310 320 330 X
TCGGCTGGATGGACAAGGGATTG
||||| ||||| ||||| ||||| |||||
TCCGCTGGATGGAGAATGCCATTG
580 590 X

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

CCTCCCCAGCTCAGGGCTGGGCCCTACAGACAGAACCCCAAGACAGAACCCAG
CCTCCCCAGCTCAGGGCTGGGCCCTACAGACAGAACCCCAAGACAGAACCCAG
80 90 100 110 120 130 140

AGTGTGAGAAGTCACACAAACCCAAAGTCTCTTGGCAGGCTTAAACCACTATCAGTCAATGGCT
AGTGTGAGAAGTCACACAAACCCAAAGTCTCTTGGCAGGCTTAAACCACTATCAGTCAATGGCT
150 160 170 180 190 200 210

TCCATAGACAGTCAGGAACTTACAGAACCTGAGAGATACGGATTGCAAGGGCTGGGG
TCCATAGGAGGCTTAAACCCAAAGTCTCTTGGCAGGCTTAAACCACTATCAGTCAATGGCT
220 230 240 250 260 270 280

ATCGGAGAGGAGTCAACGAAACTTACAGAACCTGAGAGATACGGATTGCAAGGGCTGGGG
ATCGGAGAGGAGTCAACGAAACTTACAGAACCTGAGAGATACGGATTGCAAGGGCTGGGG
290 300 310 320 330 340 350 360

CCTCAATGCTTATCTTACAACCTGTTAGCTTATCTTCGCTCTGGTGTGGAGAAGGGATTG
CCACCAATGCTTATCTTACAACCTGTTAGCTTATCTTCGCTCTGGTGTGGAGAATGGATTG
370 380 390 400 410 420 X

X 10 20 30 40 50 60 70

3. US-09-508-832-5 Sequence 5, Application US/09508832
Initial Score = 300 Optimized Score = 362 Significance = 1.49
Residue Identity = 71% Matches = 422 Mismatches = 0
Gaps = 168 Conservative Substitutions = 0

X 10 20 30 40 50 60 70

ATGGCCAAGAACCTTCTATGTAAGTCTGAGTCAGAGAACGGTGGACATTGGAGCTGCTGAGGG
ATGGCCAAGAACCTTCTATGTAAGTCTGAGTCAGAGAACGGTGGACATTGGAGCTGCTGAGGG
X 10 20 30 40 50 60 70

80 90 100 110 120

CCTCCCCAGCTCAGGGCTGGGCCCTACCTCCCTACAGACAGAACCCCAAGGTTAACCGCAGGGAAAGGG
CCTCCCCAGCTCAGGGCTGGGCCCTACCTCCCTACAGACAGAACCCCAAGGTTAACCGCAGGGAAAGGG
80 90 100 110 120 130 140

130 140 150 160 170 180 190

-AGACAGGAGCCGGCACCCATGAGTGTGAGAAGATCTTCCTGCTGCTGGTATTTCCTCTTGAC
ACAGACAGGAGCCGGCACCCATGAGTGTGAGAAGATCTTCCTGCTGCTGGTATTTCCTCTTGAC
220 230 240 250 260 270 280

200 210 220 230 240 250 260

AACCACTATCTCAGTCAGTCAGGAGGAACTTCAGGAGTCACACAAACCCCAACTCCMCCATTGCCAGGGATA
AACCACTATCTCAGTCAGTCAGGAGGAACTTCAGGAGTCACACAAACCCCAACTCCMCCATTGCCAGGGATA
290 300 310 320 330 340 350 360

270 280 290 300 310 320 330

CGGATTCAGGAGGCTGGCTGGGAGATCGAGGAGTCACAGAACCTGAGGTTATCTCCTGCTGCTGCTGGTATTTCCTCTTGAC
GATTACCCGAGCTGGCTGAAGACCACTCCATTGGTATCTCCTGCTGCTGGTATTTCCTCTTGAC
510 520 530 540 550 560 570

410 420 X

TGAGAAGGGCATG
TGAGAAGGGCATG
580 590

4. US-09-508-832-3 (1-422) Sequence 9, Application US/09508832
Initial Score = 245 Optimized Score = 295 Significance = 1.10
Residue Identity = 60% Matches = 365 Mismatches = 51
Gaps = 186 Conservative Substitutions = 0

X 10 20 30 40 50 60 70

ATGGCCAGGAACTTCTGATGTAAGTCTGAGTCAGAGAACGGTGGACATTGGAGCTGCTGAGGG
ATGGCCAGGAACTTCTGATGTAAGTCTGAGTCAGAGAACGGTGGACATTGGAGCTGCTGAGGG
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140

CCCTCCCAGCTGCTGGGCCCTAACCTCCCTACAGACAGAACCCCAAGGTTAACCGCAGGGAAAGGG
CCCTCCCAGCTGCTGGGCCCTAACCTCCCTACAGACAGAACCCCAAGGTTAACCGCAGGGAAAGGG
150 160 170 180 190 200 210

190 200 210 220 230 240 250

TGCAAGGGATACCCATGAGTCAGGAGTCACAGAACCTGAGGTTAACCGCAGGGAAAGGG
TGCAAGGGATACCCATGAGTCAGGAGTCACAGAACCTGAGGTTAACCGCAGGGAAAGGG
290 300 310 320 330 340 350 360

330 340 350 360 370 380 390

CGCCGGAGATAGGATGCAAGGAGTCAGGAGTCACAGAACCTGAGGTTAACCGCAGGGAAAGGG
CGCCGGAGATAGGATGCAAGGAGTCAGGAGTCACAGAACCTGAGGTTAACCGCAGGGAAAGGG
430 440 450 460 470 480 490

500 510 520 530 540 550 560 570

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)